

Figure 1

SEQUENCE LISTING

5 <110> WARNER-LAMBERT

<120> Matrix metalloproteinase inhibitors

<130> A0000434

10 <140>

<141>

<160> 1

15 <170> PatentIn Ver. 2.1

<210> 1

<211> 471

20 <212> PRT

<213> Homo sapiens

<400> 1

25	Met	His	Pro	Gly	Val	Leu	Ala	Ala	Phe	Leu	Phe	Leu	Ser	Trp	Thr	His	
	1				5					10					15		
	Cys	Arg	Ala	Leu	Pro	Leu	Pro	Ser	Gly	Gly	Asp	Glu	Asp	Asp	Leu	Ser	
				20					25					30			
30	Glu	Glu	Asp	Leu	Gln	Phe	Ala	Glu	Arg	Tyr	Leu	Arg	Ser	Tyr	Tyr	His	
			35					40					45				
	Pro	Thr	Asn	Leu	Ala	Gly	Ile	Leu	Lys	Glu	Asn	Ala	Ala	Ser	Ser	Met	
		50					55					60					
35	Thr	Glu	Arg	Leu	Arg	Glu	Met	Gln	Ser	Phe	Phe	Gly	Leu	Glu	Val	Thr	
	65				70						75				80		
	Gly	Lys	Leu	Asp	Asp	Asn	Thr	Leu	Asp	Val	Met	Lys	Lys	Pro	Arg	Cys	
40				85					90						95		
	Gly	Val	Pro	Asp	Val	Gly	Glu	Tyr	Asn	Val	Phe	Pro	Arg	Thr	Leu	Lys	
			100						105					110			
45	Trp	Ser	Lys	Met	Asn	Leu	Thr	Tyr	Arg	Ile	Val	Asn	Tyr	Thr	Pro	Asp	
			115					120					125				
	Met	Thr	His	Ser	Glu	Val	Glu	Lys	Ala	Phe	Lys	Lys	Ala	Phe	Lys	Val	
		130					135					140					
50	Trp	Ser	Asp	Val	Thr	Pro	Leu	Asn	Phe	Thr	Arg	Leu	His	Asp	Gly	Ile	
	145					150					155				160		
	Ala	Asp	Ile	Met	Ile	Ser	Phe	Gly	Ile	Lys	Glu	His	Gly	Asp	Phe	Tyr	
55				165						170					175		
	Pro	Phe	Asp	Gly	Pro	Ser	Gly	Leu	Leu	Ala	His	Ala	Phe	Pro	Pro	Gly	
				180					185						190		

5 Pro Asn Tyr Gly Gly Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
 195 200 205
 Ser Ser Ser Lys Gly Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe
 210 215 220
 10 Gly His Ser Leu Gly Leu Asp His Ser Lys Asp Pro Gly Ala Leu Met
 225 230 235 240
 Phe Pro Ile Tyr Thr Tyr Thr Gly Lys Ser His Phe Met Leu Pro Asp
 245 250 255
 15 Asp Asp Val Gln Gly Ile Gln Ser Leu Tyr Gly Pro Gly Asp Glu Asp
 260 265 270
 20 Pro Asn Pro Lys His Pro Lys Thr Pro Asp Lys Cys Asp Pro Ser Leu
 275 280 285
 Ser Leu Asp Ala Ile Thr Ser Leu Arg Gly Glu Thr Met Ile Phe Lys
 290 295 300
 25 Asp Arg Phe Phe Trp Arg Leu His Pro Gln Gln Val Asp Ala Glu Leu
 305 310 315 320
 Phe Leu Thr Lys Ser Phe Trp Pro Glu Leu Pro Asn Arg Ile Asp Ala
 325 330 335
 30 Ala Tyr Glu His Pro Ser His Asp Leu Ile Phe Ile Phe Arg Gly Arg
 340 345 350
 Lys Phe Trp Ala Leu Asn Gly Tyr Asp Ile Leu Glu Gly Tyr Pro Lys
 355 360 365
 35 Lys Ile Ser Glu Leu Gly Leu Pro Lys Glu Val Lys Lys Ile Ser Ala
 370 375 380
 40 Ala Val His Phe Glu Asp Thr Gly Lys Thr Leu Leu Phe Ser Gly Asn
 385 390 395 400
 Gln Val Trp Arg Tyr Asp Asp Thr Asn His Ile Met Asp Lys Asp Tyr
 405 410 415
 45 Pro Arg Leu Ile Glu Glu Asp Phe Pro Gly Ile Gly Asp Lys Val Asp
 420 425 430
 Ala Val Tyr Glu Lys Asn Gly Tyr Ile Tyr Phe Phe Asn Gly Pro Ile
 435 440 445
 50 Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro
 450 455 460
 55 Ala Asn Ser Ile Leu Trp Cys
 465 470

Figure 2

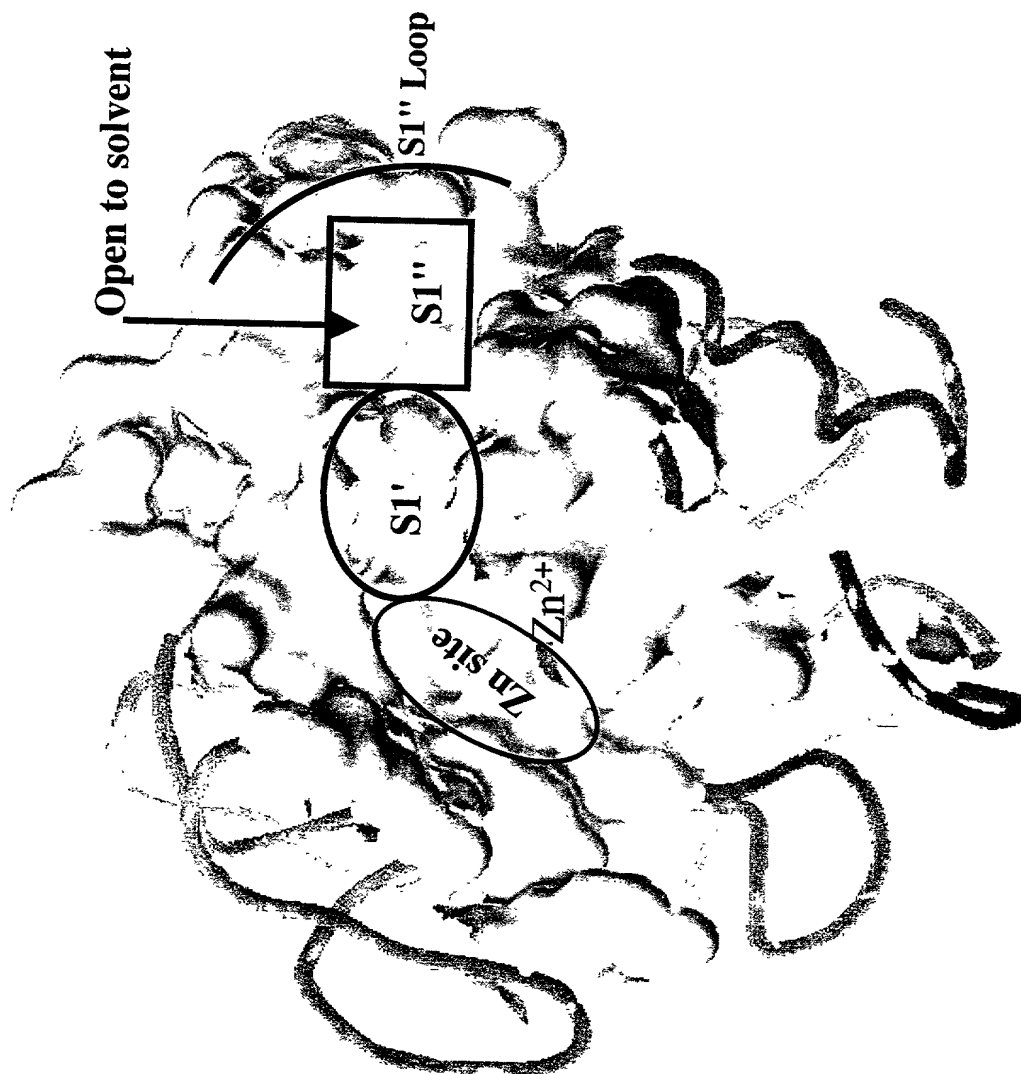


Figure 3: Synthesis example 1 binding mode

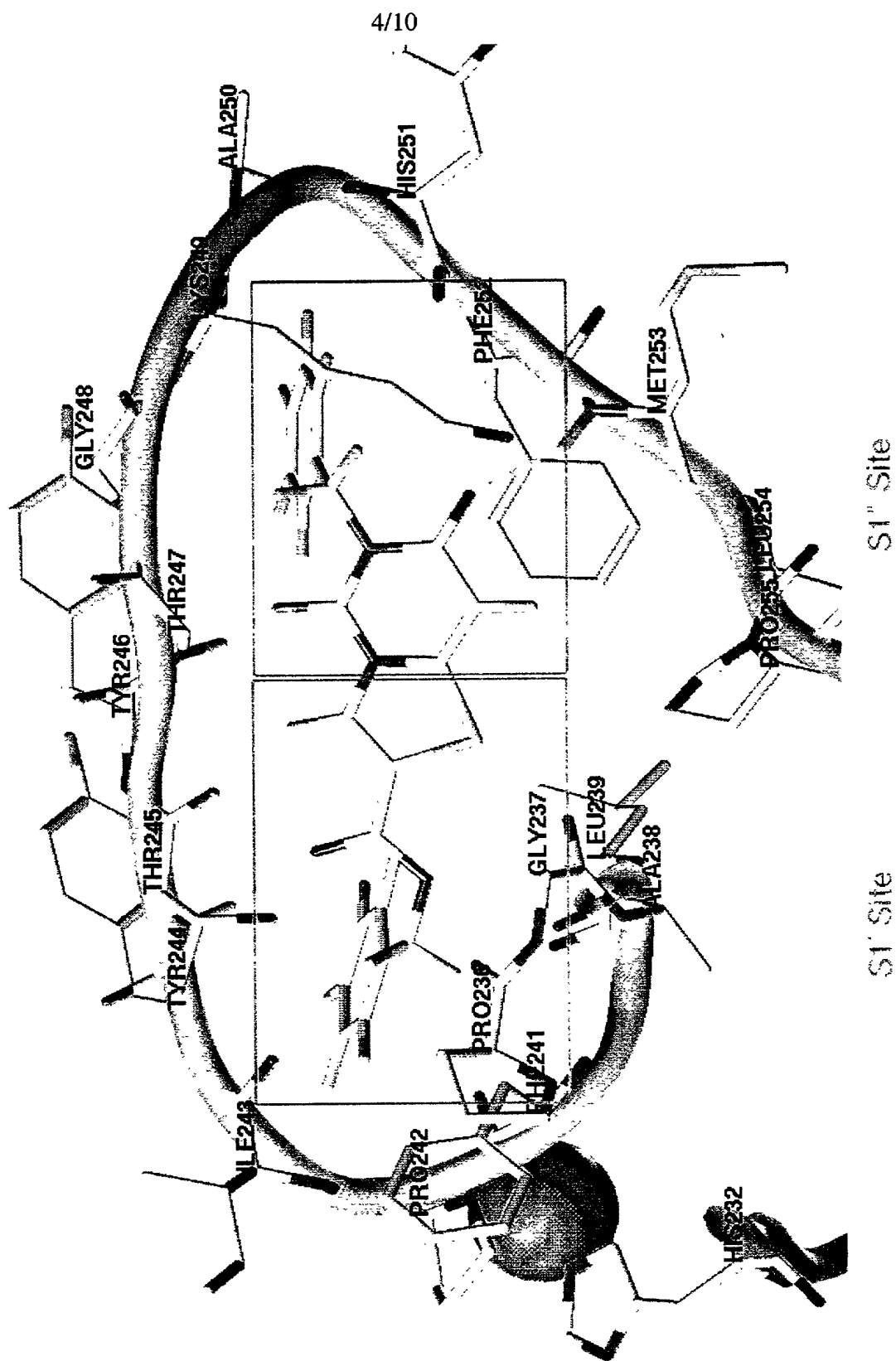


Figure 4: Synthesis example 1 binding mode

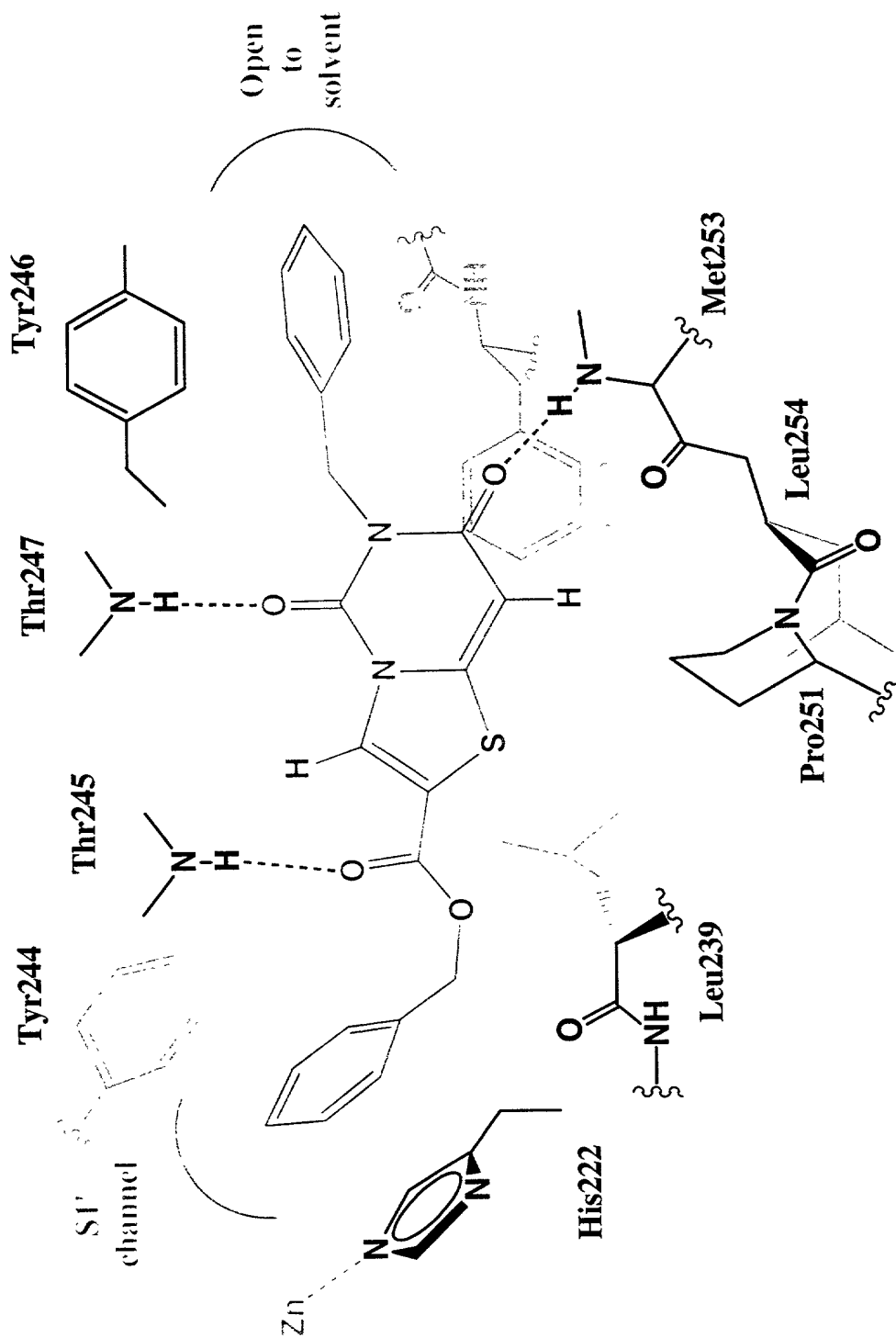


Figure 5: Synthesis example 10 binding mode

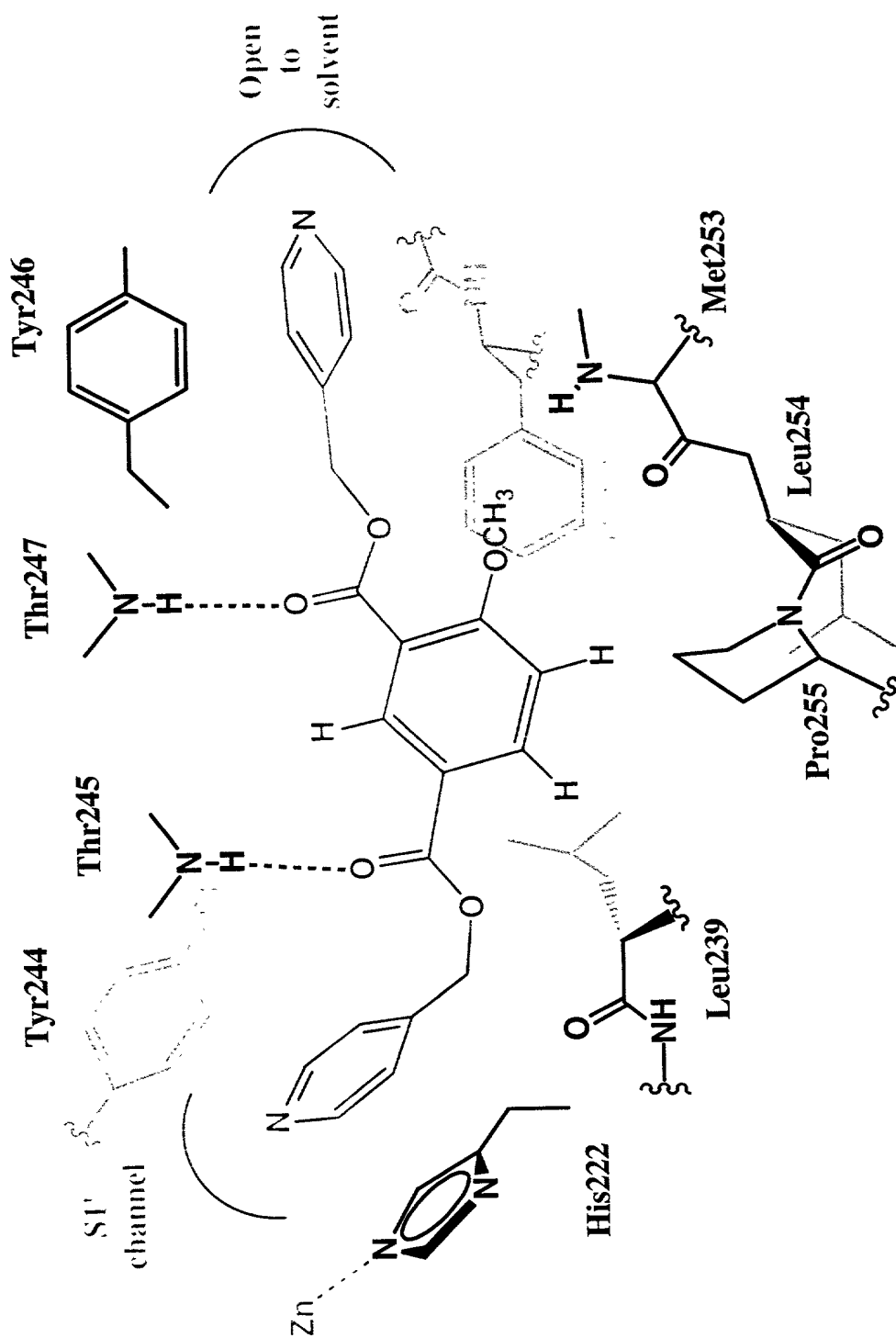


Figure 6: fused Bicyclic Pyrimidones-binding mode

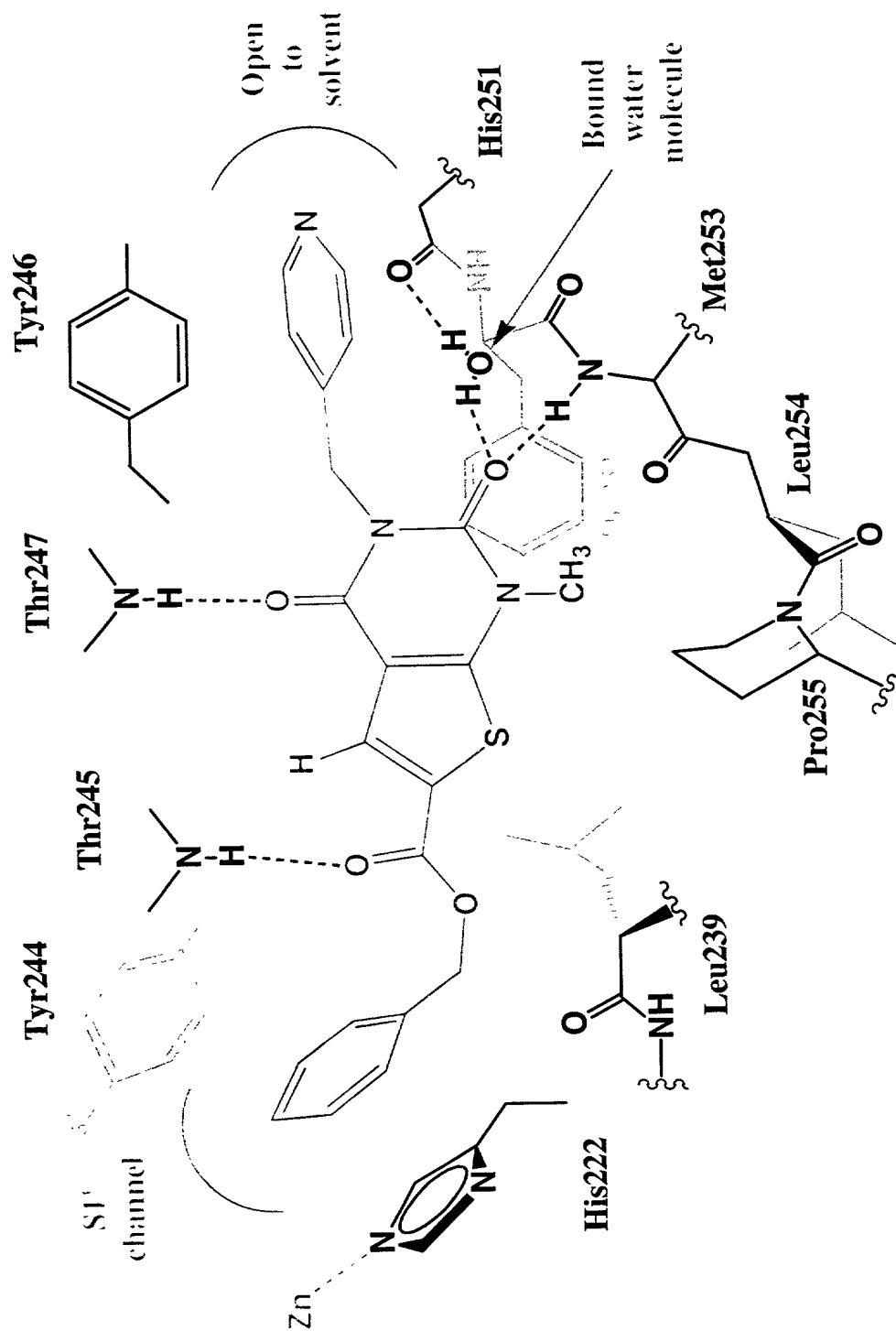


Figure 7: Synthesis example 39 binding mode

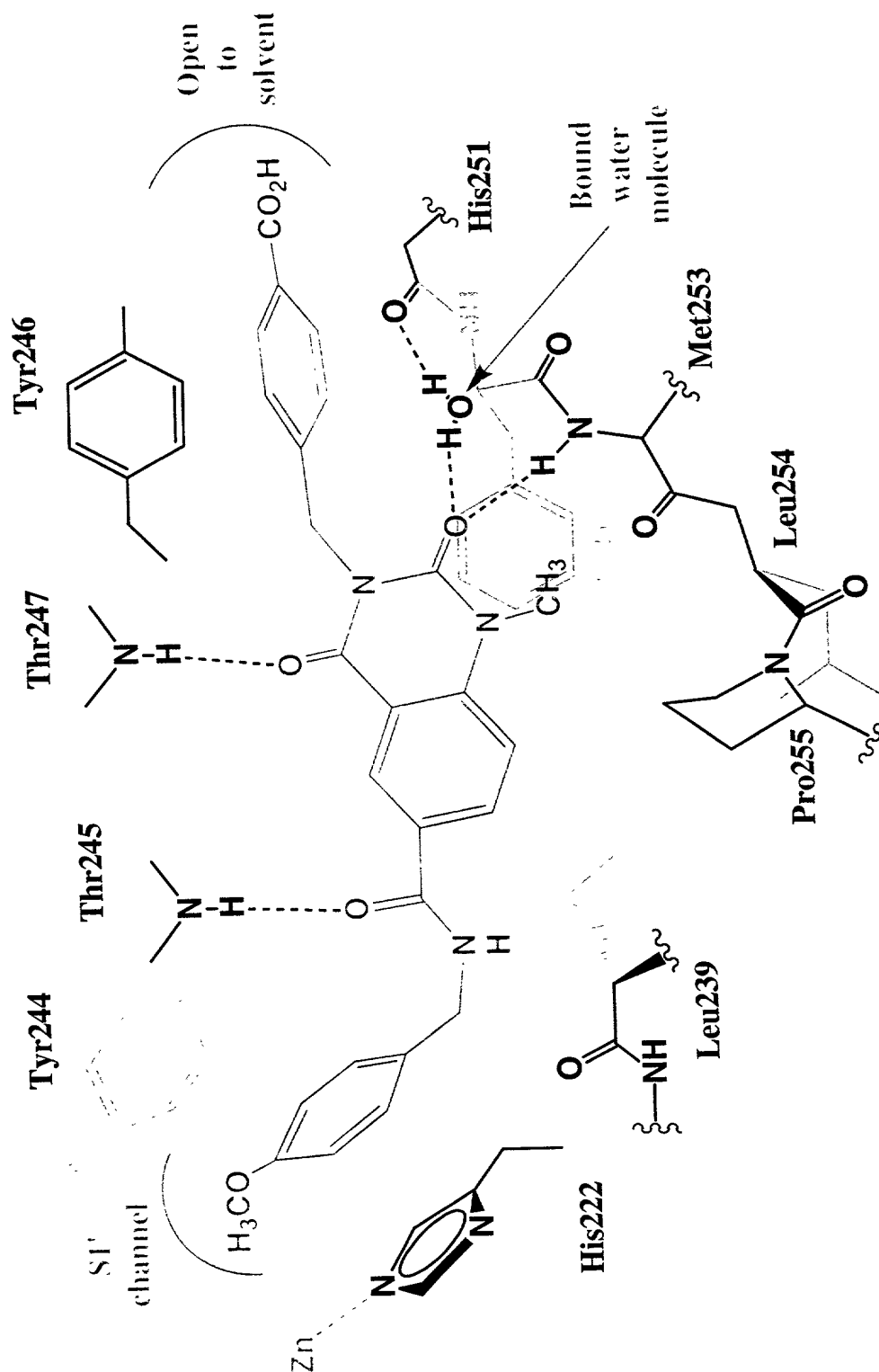


Figure 8: Synthesis example 57 binding mode

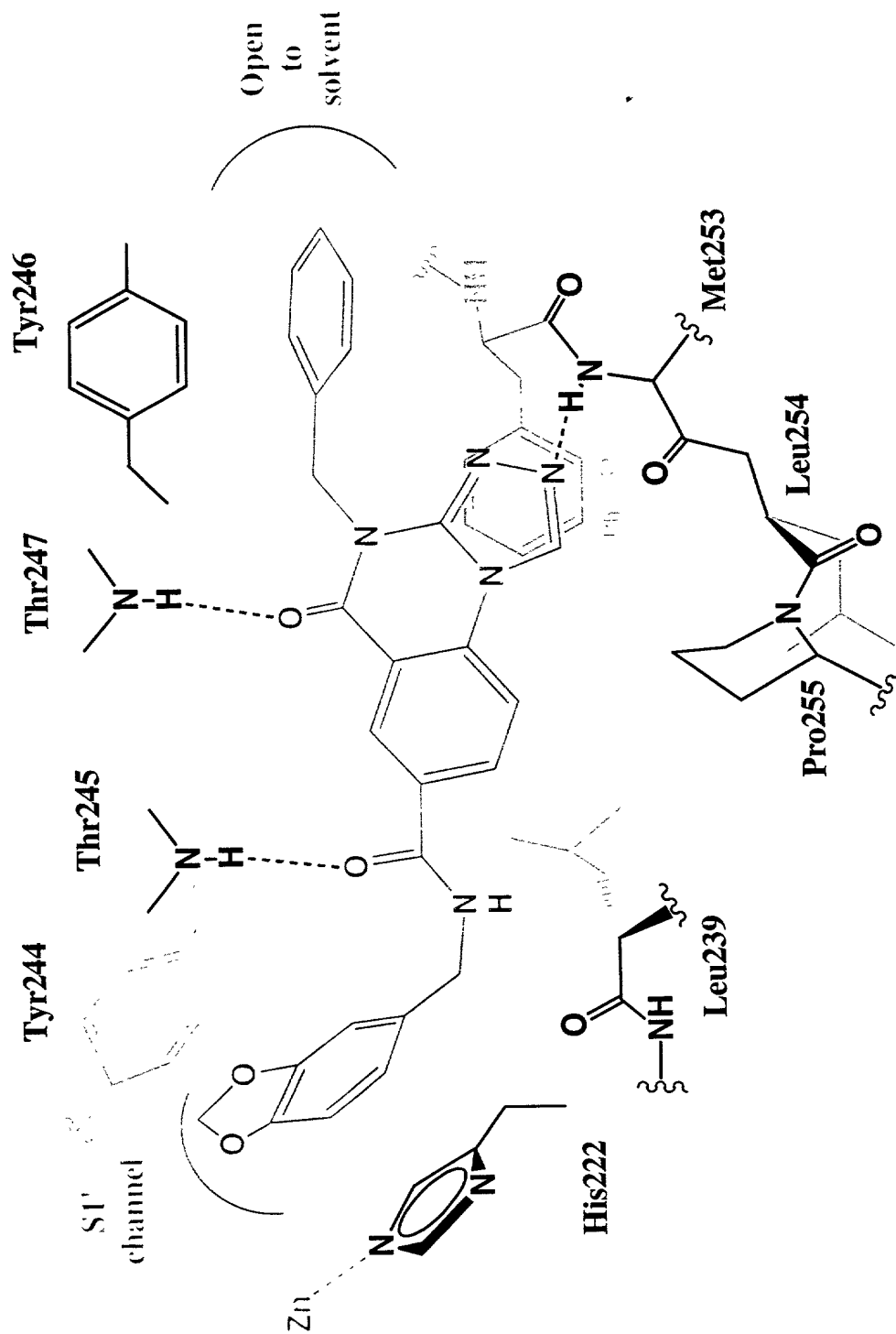


Figure 9 : Coordinates in the space of the hydrophobic groups and hydrogen bond acceptors of the pharmacophore

